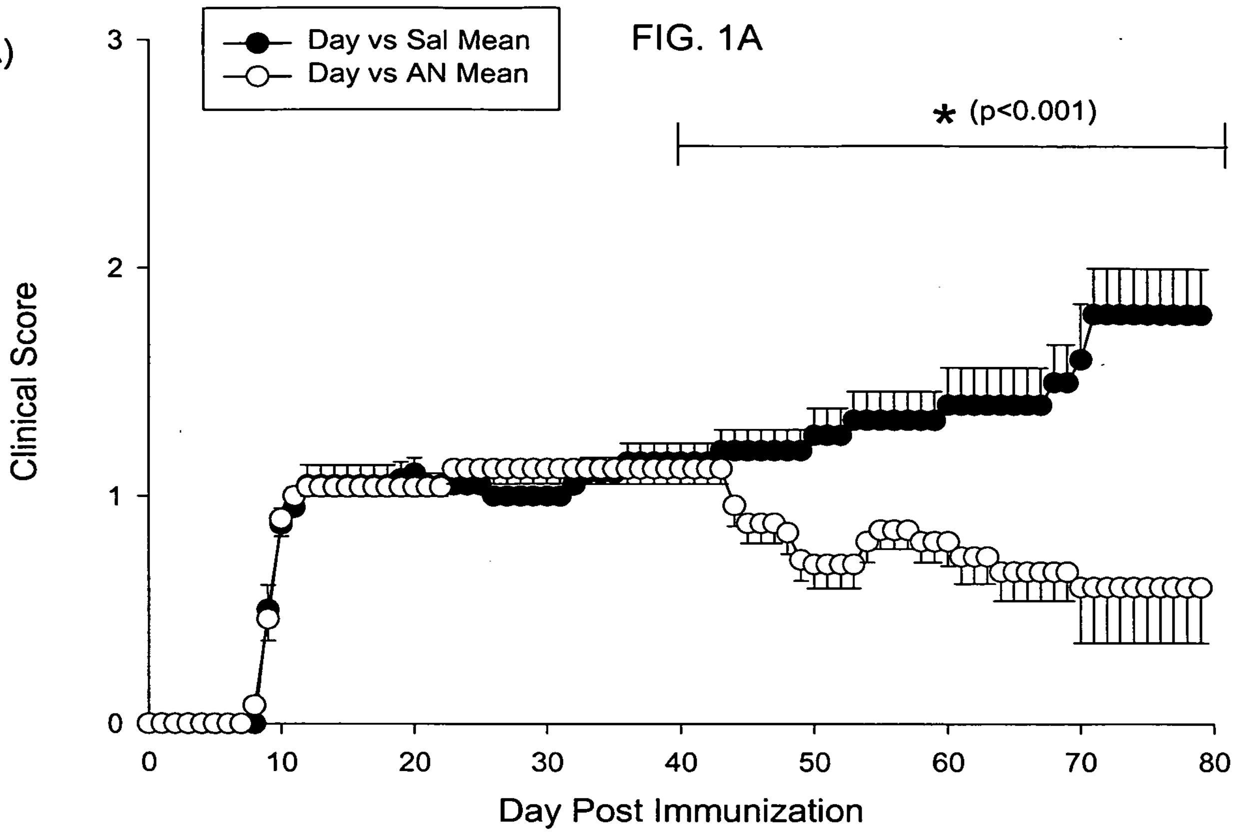
(A)


Day vs Sal Mean
Day vs AN Mean
FIG. 1A
* (p<0.001)
Clinical Score
0
1
2
3
0
10
20
30
40
50
60
70
80
Day Post Immunization

(B)

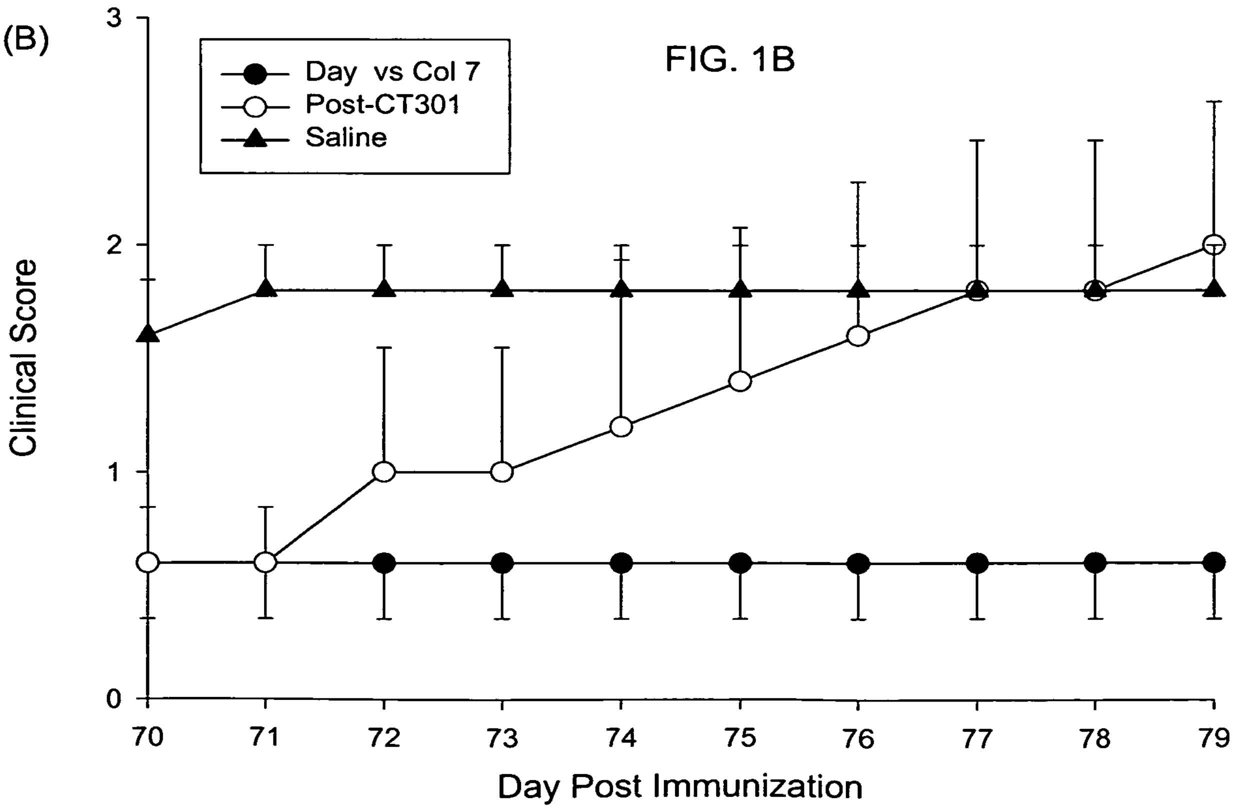

Day vs Col 7
Post-CT301
Saline
FIG. 1B
Clinical Score
0
1
2
3
70
71
72
73
74
75
76
77
78
79
Day Post Immunization

FIG. 2G

FIG. 2H

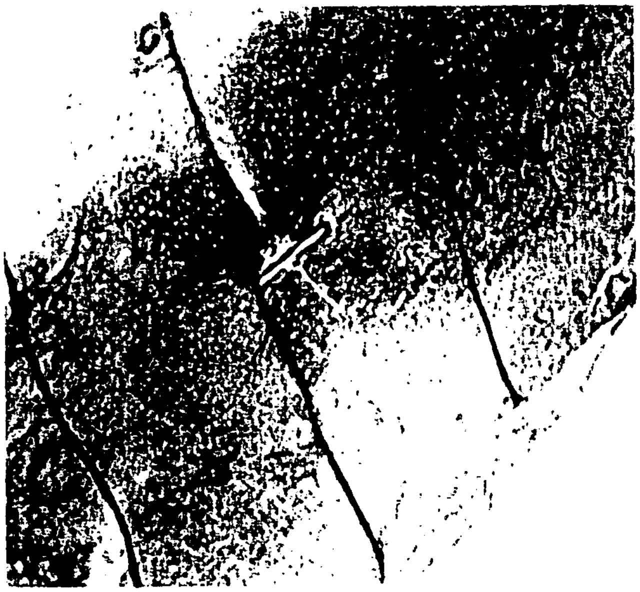


FIG. 2I

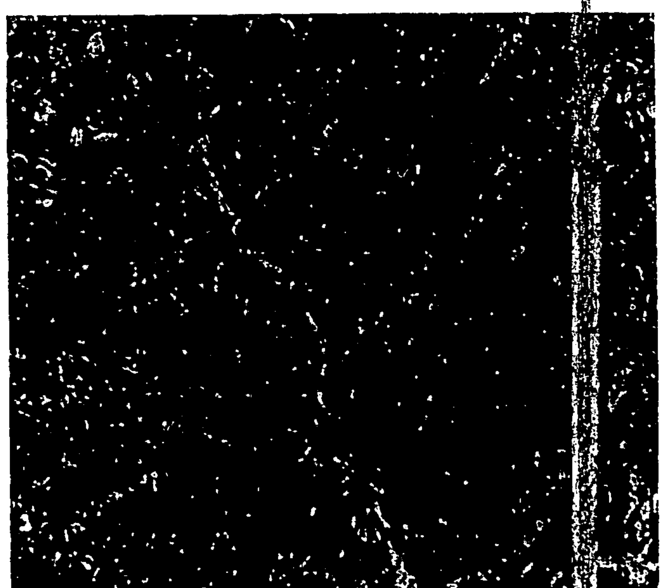


FIG. 2J

FIG. 2K

FIG. 2L

FIG. 2A

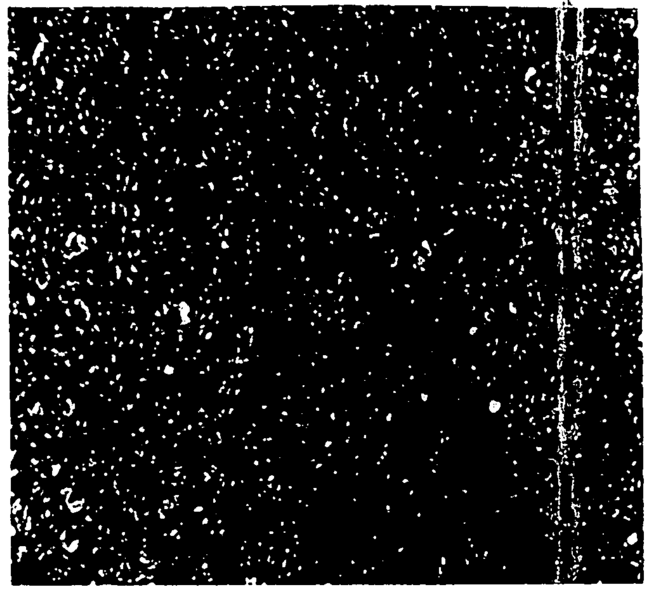


FIG. 2B

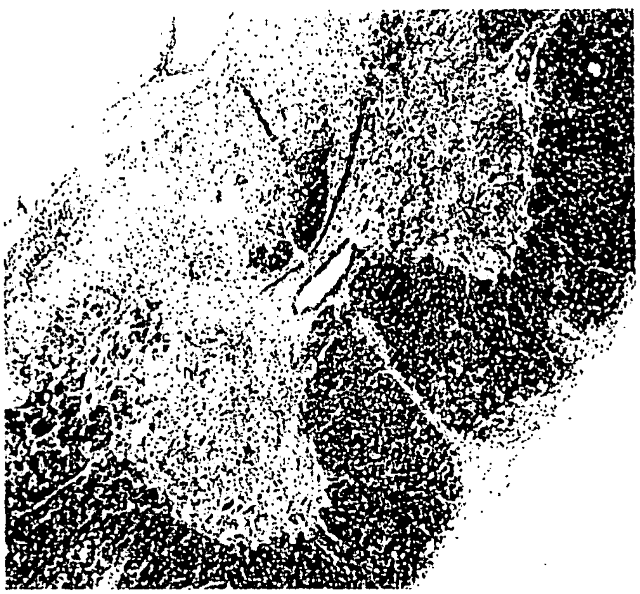


FIG. 2C

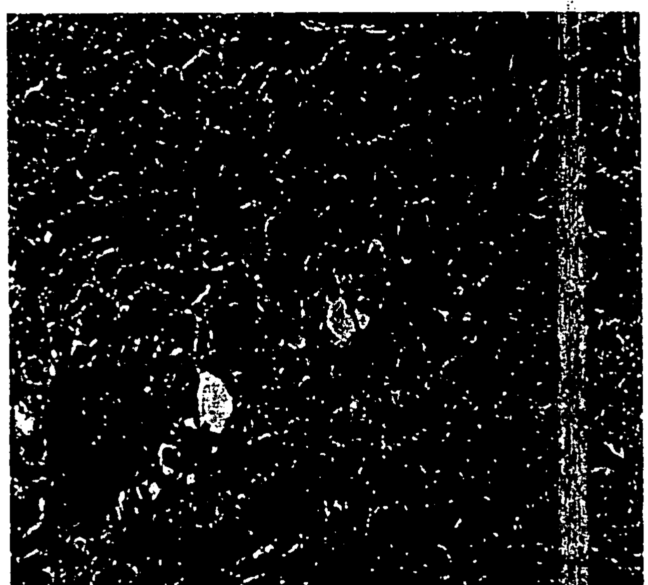


FIG. 2D

FIG. 2E

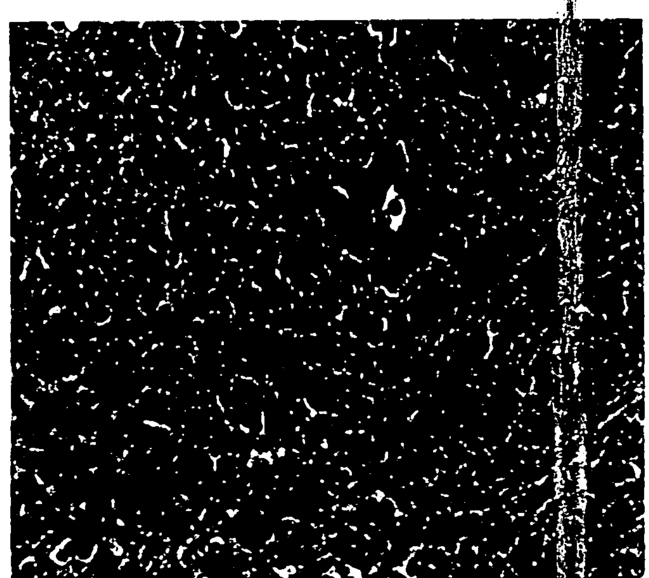


FIG. 2F

FIG. 3A

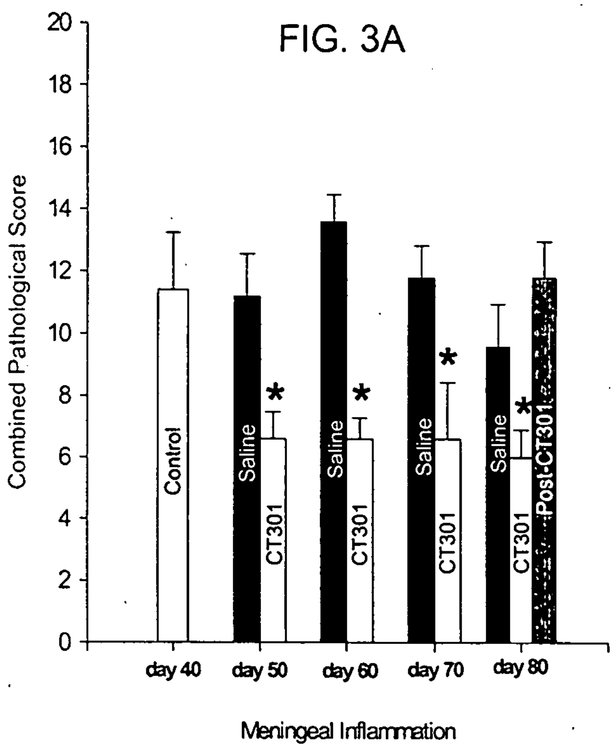


FIG. 3B

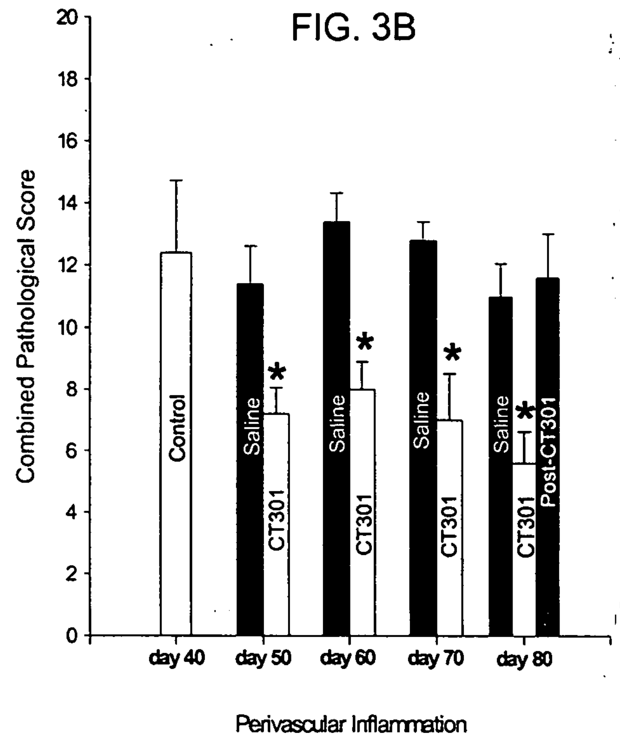


FIG. 3C

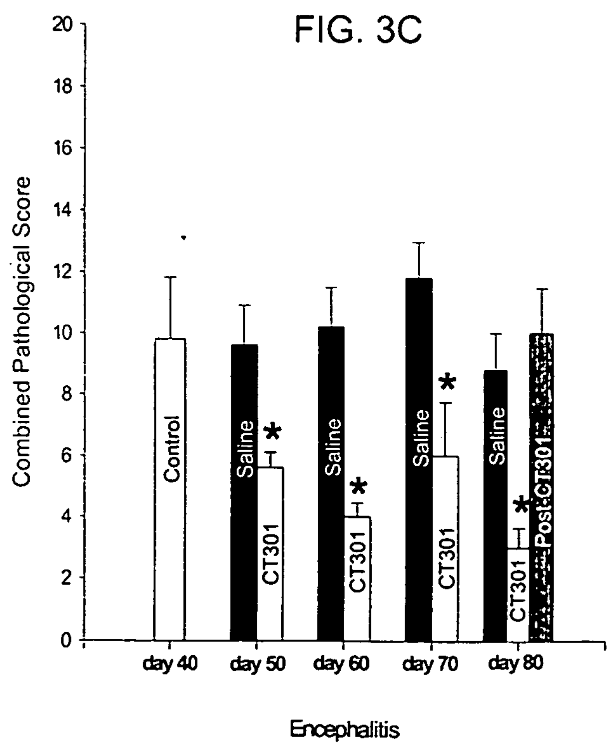
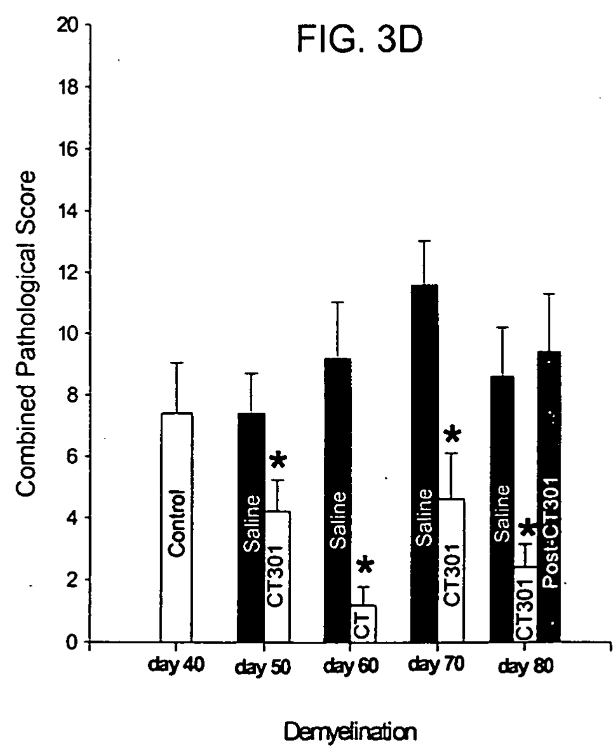


FIG. 3D



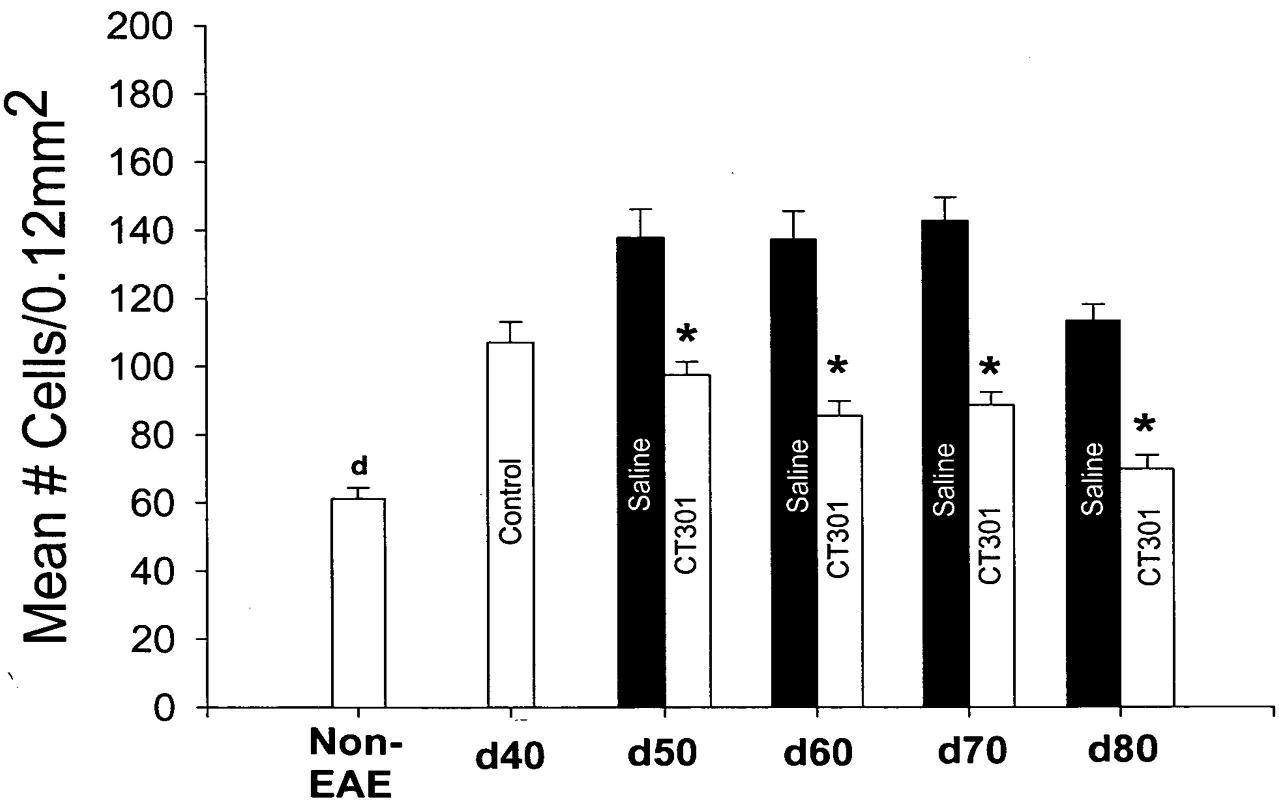

Mean # Cells/0.12mm2
200
180
160
140
120
100
80
60
40
20
0
d
Control
Saline
CT301
*
Non-EAE
d40
d50
d60
d70
d80

FIG. 4

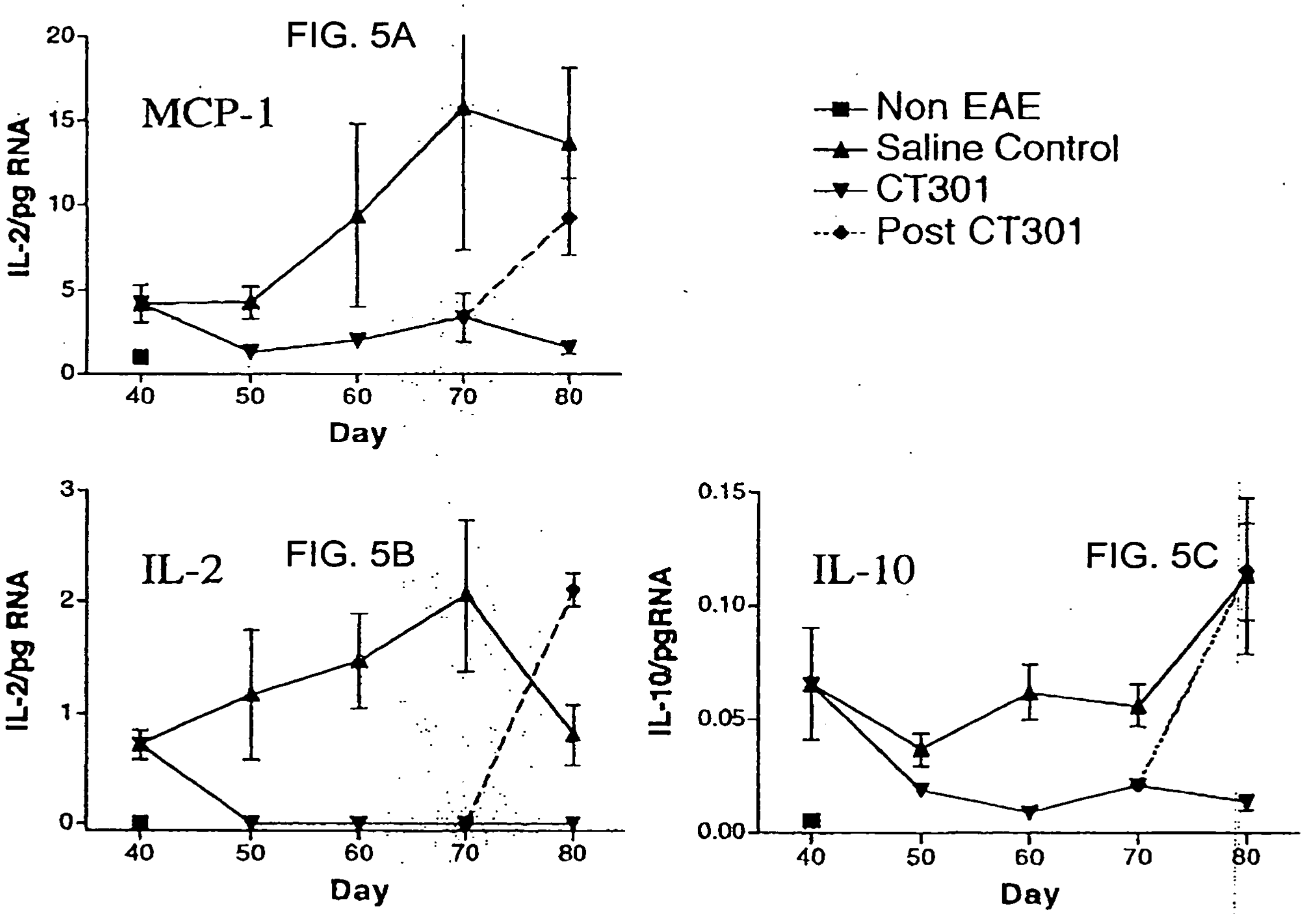
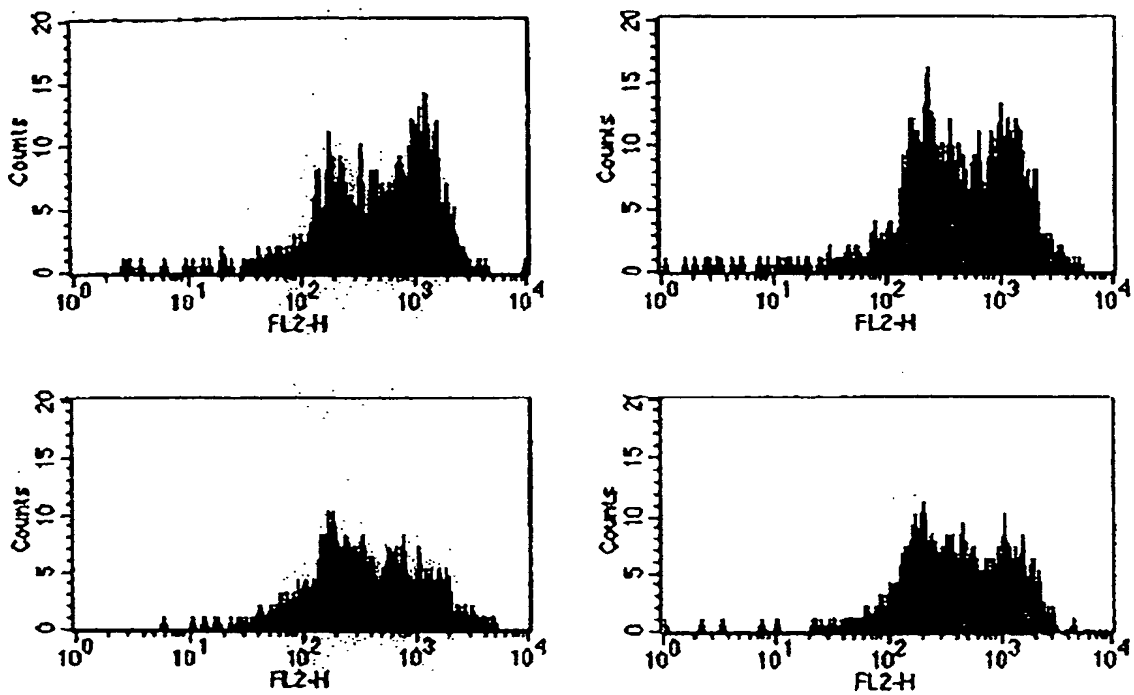


FIG. 5A
MCP-1
IL-2/pg RNA
20
15
10
5
0
40
50
60
70
80
Day
Non EAE
Saline Control
CT301
Post CT301
FIG. 5B
IL-2
IL-2/pg RNA
3
2
1
0
40
50
60
70
80
Day
FIG. 5C
IL-10
IL-10/pgRNA
0.15
0.10
0.05
0.00
40
50
60
70
80
Day

CT301



Saline

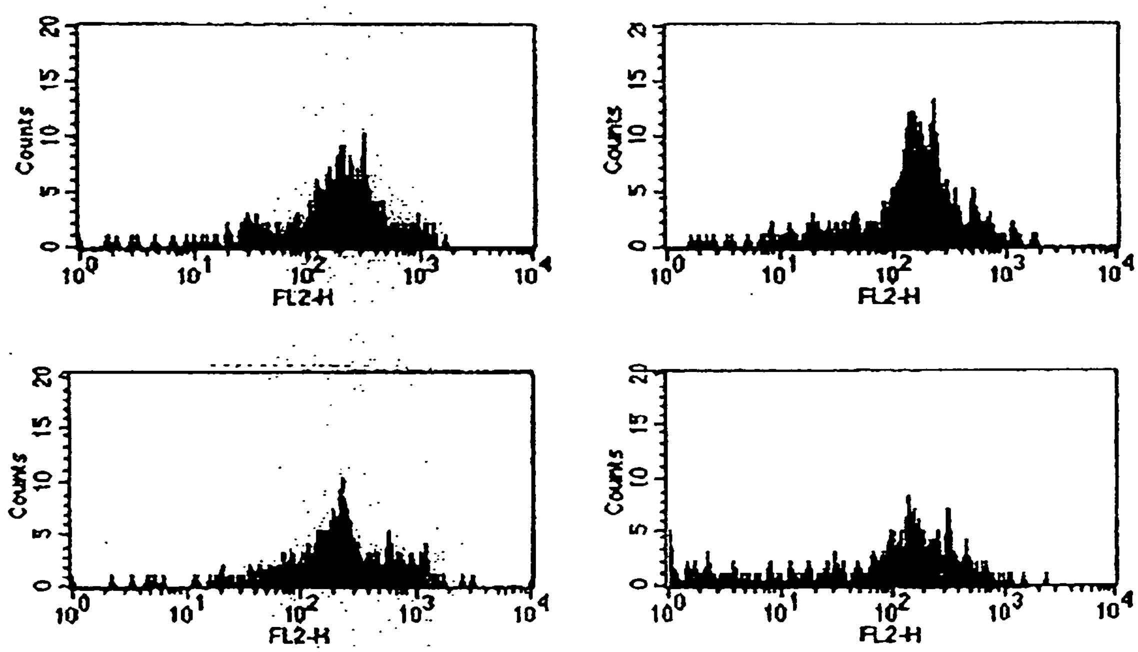


FIG. 6

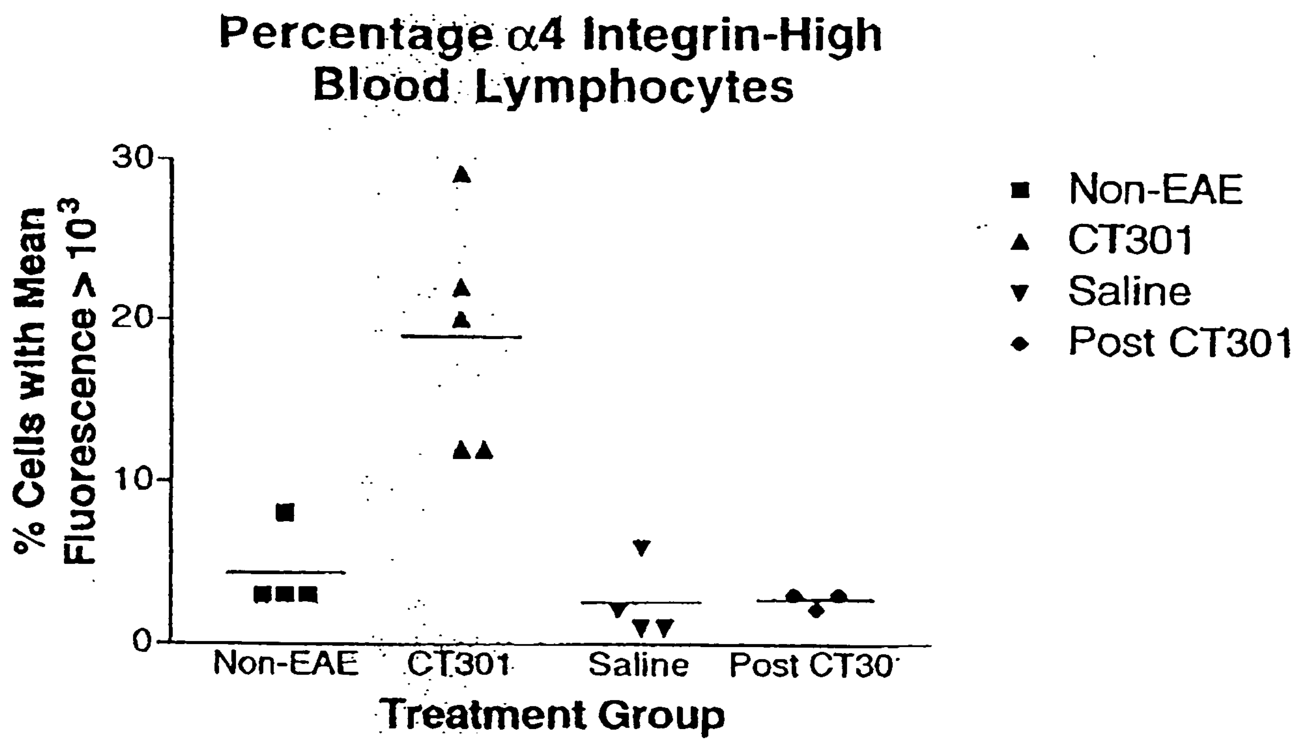

Percentage α4 Integrin-High Blood Lymphocytes
% Cells with Mean Fluorescence > 10^3
30
20
10
0
Non-EAE
CT301
Saline
Post CT301
Non-EAE
CT301
Saline
Post CT30
Treatment Group

FIG. 7A

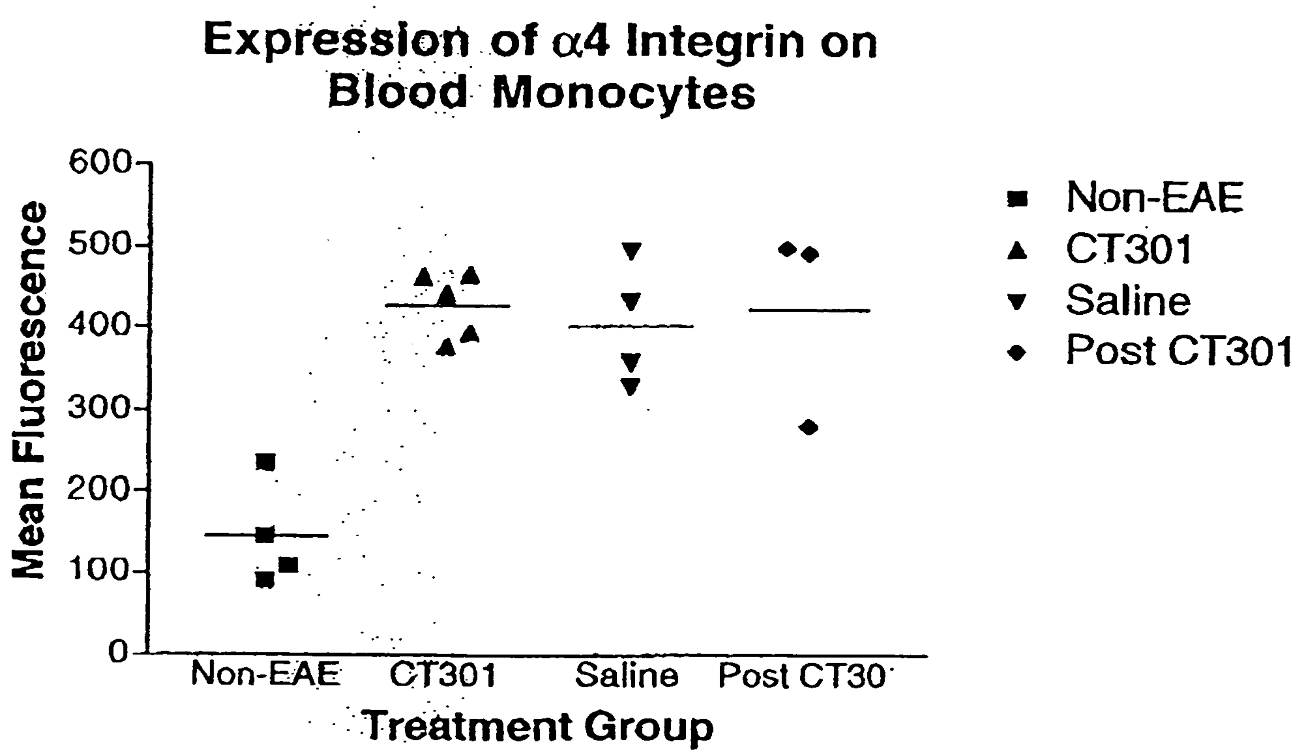

Expression of α4 Integrin on Blood Monocytes
Mean Fluorescence
600
500
400
300
200
100
0
Non-EAE
CT301
Saline
Post CT301
Non-EAE
CT301
Saline
Post CT30
Treatment Group

FIG. 7B

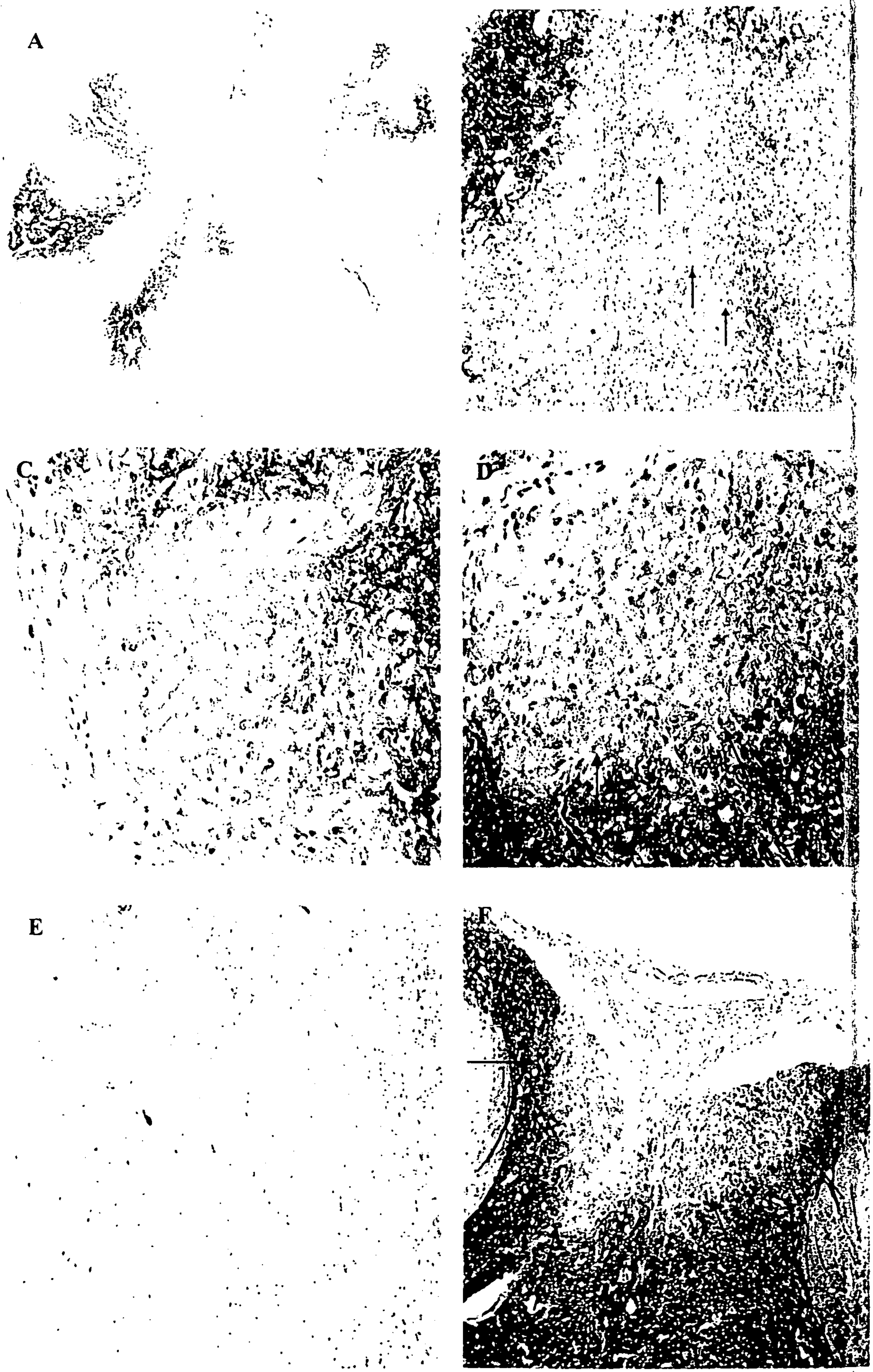


FIG. 8

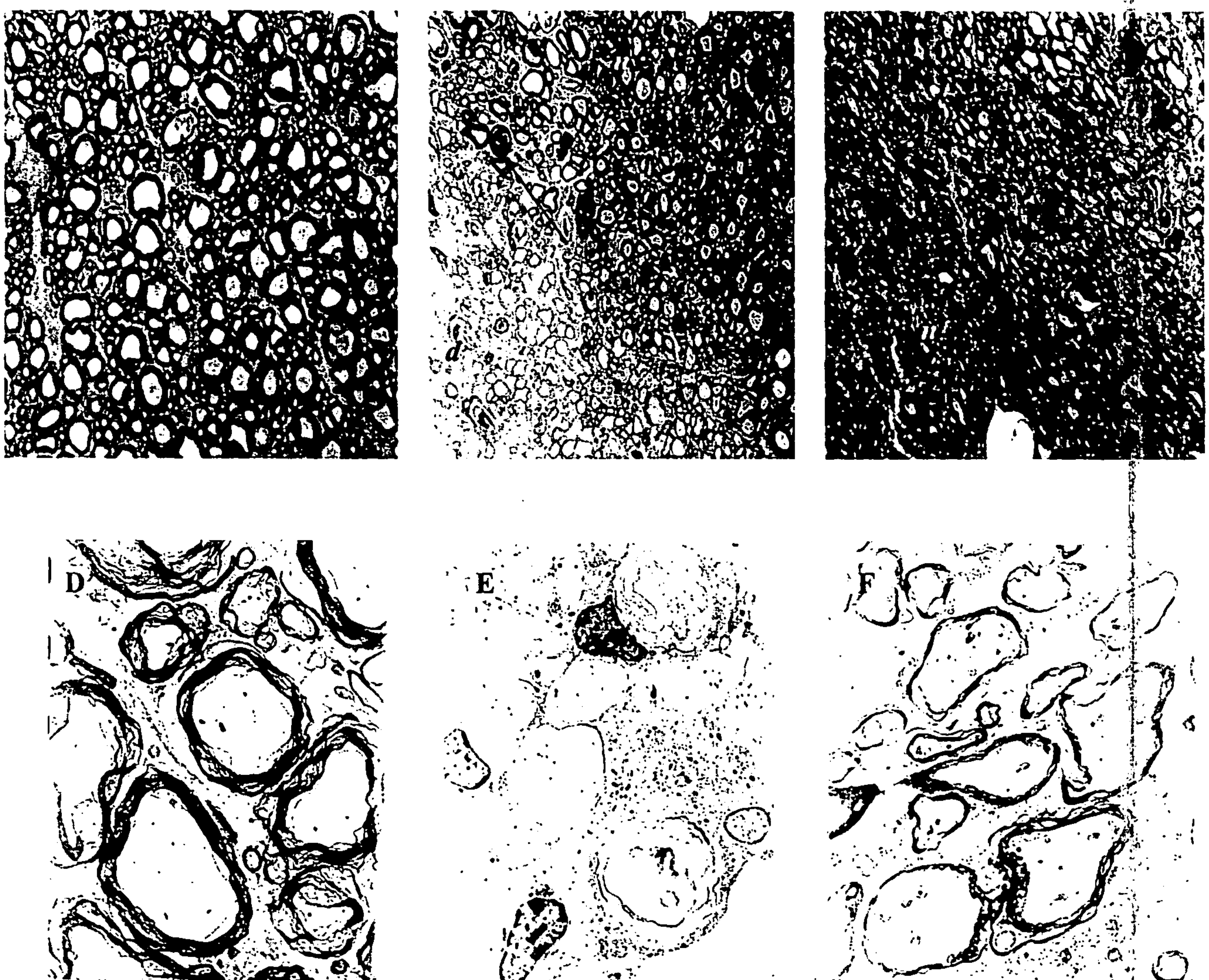


FIG. 9

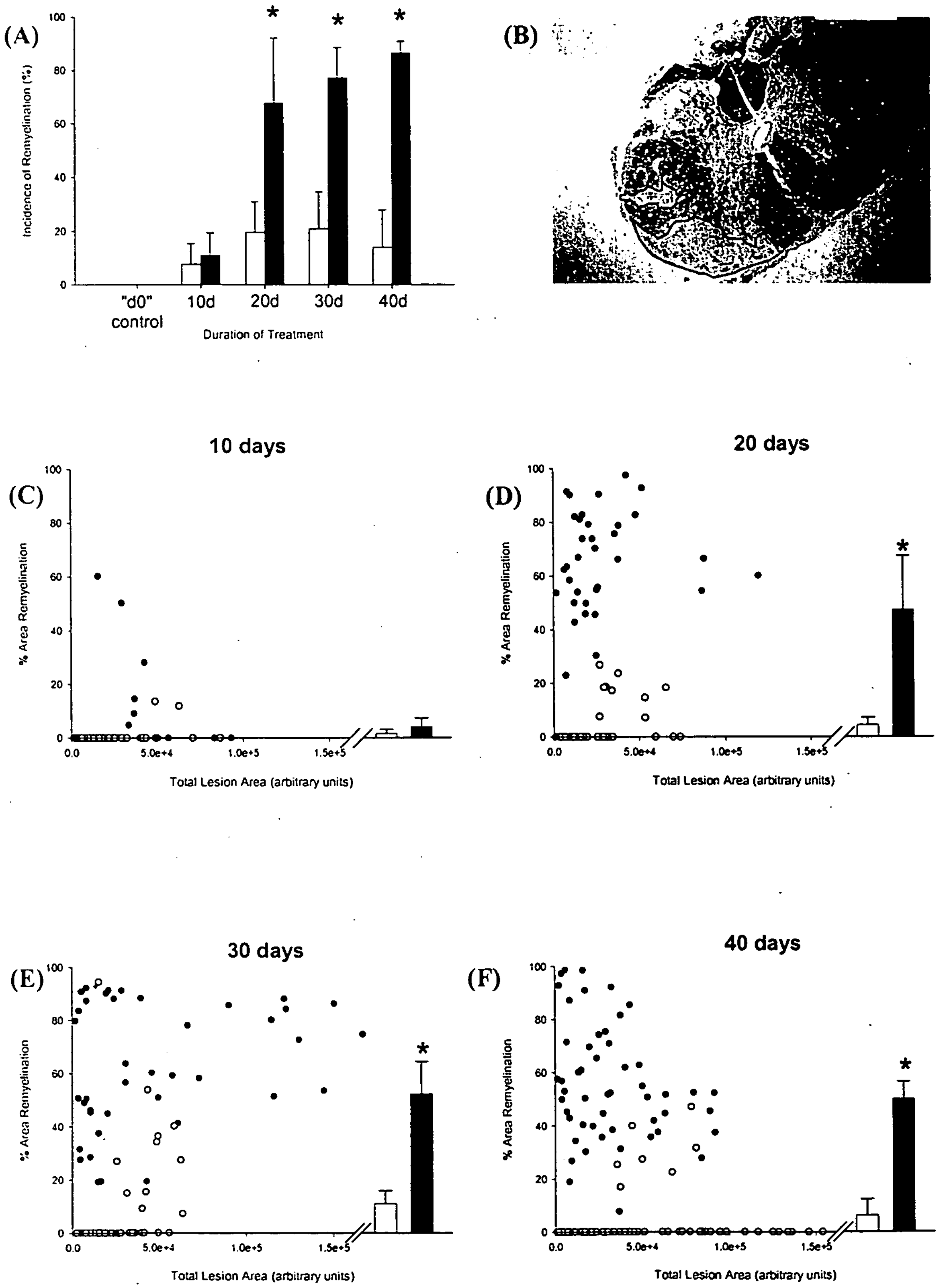

(A)
Incidence of Remyelination (%)
100
80
60
40
20
0
*
*
*
"d0"
control
10d
20d
30d
40d
Duration of Treatment
(B)
10 days
(C)
% Area Remyelination
Total Lesion Area (arbitrary units)
0.0
5.0e+4
1.0e+5
1.5e+5
20 days
(D)
30 days
(E)
40 days
(F)

FIG. 10

```
   atgagggcccctgctcagattttggattcttggtcaggagacgttgt
1  -----------------------------------------------
   tactccccggggacgagtctaaaacctaagaaccagtcctctgcaaca

   agaaatgagaccgtctattcagttcctggggctcttgttgttctggcttcatgg
49 ------------------------------------------------------
   tctttactctggcagataagtcaaggaccccgagaacaacaagaccgaagtacc

    [M  R  P  S  I  Q  F  L  G  L  L  L  F  W  L  H  G
                           LEADER

    tgctcagtgtgacatccagatgacacagtctccatcctcactgtctgcatctct
103 ------------------------------------------------------
    acgagtcacactgtaggtctactgtgtcagaggtaggagtgacagacgtagaga

    A  Q  C] [D  I  Q  M  T  Q  S  P  S  S  L  S  A  S  L
                                              FR1
    gggaggcaaagtcaccatcacttgcaagacaagccaagacattaacaagtatat
157 ------------------------------------------------------
    ccctccgtttcagtggtagtgaacgttctgttcggttctgtaattgttcatata

    G  G  K  V  T  I  T  C] [K  T  S  Q  D  I  N  K  Y  M
                                        CDR1
    ggcttggtaccaacacaagcctggaaaacgtcctaggctgctcatacattacac
211 ------------------------------------------------------
    ccgaaccatggttgtgttcggacctttgcaggatccgacgagtatgtaatgtg

    A] [W  Y  Q  H  K  P  G  K  R  P  R  L  L  I  H] [Y  T
                          FR2
    atctgcattacagccaggcatcccatcaaggttcagtggaagtgggtctgggag
265 ------------------------------------------------------
    tagacgtaatgtcggtccgtagggtagttccaagtcaccttcacccagaccctc

    S  A  L  Q  P] [G  I  P  S  R  F  S  G  S  G  S  G  R
     CDR2
```

FIG. 11 A

```
    agattattccttcaacatcagcaacctggagcctgaagatattgcaacttatta
319 ------------------------------------------------------
    tctaataaggaagttgtagtcgttggacctcggacttctataacgttgaataat

     D  Y  S  F  N  I  S  N  L  E  P  E  D  I  A  T  Y  Y
       FR3

    ttgtctacagtatgataatctgtggacgttcggtggaggcaccaagctggaaat
373 ------------------------------------------------------
    aacagatgtcatactattagacacctgcaagccacctccgtggttcgaccttta

     C][L  Q  Y  D  N  L  W  T][F  G  G  G  T  K  L  E  I
             CDR3                          FR4

    caaacgggctgatgctgcaccaactgtatccatcttcccaccatccacccggga
427 ------------------------------------------------------
    gtttgcccgactacgacgtggttgacataggtagaagggtggtaggtgggccct

     K]

    AGG-5'
    tcc
481 ---
    agg
```

FIG. 11B

```
      atgaaatgcagctgggtcatgttcttcctgatggcagtggttacaggg
  1   ------------------------------------------------
      tactttacgtcgacccagtacaagaaggactaccgtcaccaatgtccc

      [M  K  C  S  W  V  M  F  F  L  M  A  V  V  T  G
                          LEADER

      gtcaattcagaggttcagctgcagcagtctggggcagagcttgtgaagccaggg
 49   ------------------------------------------------------
      cagttaagtctccaagtcgacgtcgtcagaccccgtctcgaacacttcggtccc

      V  N  S][E  V  Q  L  Q  Q  S  G  A  E  L  V  K  P  G
                                                FR1

      gcctcagtcaagttgtcctgcacagcttctggcttcaacattaaagacacctat
103   ------------------------------------------------------
      cggagtcagttcaacaggacgtgtcgaagaccgaagttgtaatttctgtggata

      A  S  V  K  L  S  C  T  A  S  G  F  N  I  K][D  T  Y
                                                     CDR1

      atacactgtgtgaagcagaggcctgaacagggcctggagtggattggaaggatt
157   ------------------------------------------------------
      tatgtgacacacttcgtctccggacttgtcccggacctcacctaaccttcctaa

      I  H][C  V  K  Q  R  P  E  Q  G  L  E  W  I  G][R  I
                                 FR2

      gatcctgcgaatggttatactaaatatgacccgaagttccagggcaaggccact
211   ------------------------------------------------------
      ctaggacgcttaccaatatgatttatactgggcttcaaggtcccgttccggtga

      D  P  A  N  G  Y  T  K  Y  D  P  K  F  Q  G][K  A  T
                     CDR2

      ataacagctgacacatcctccaacacagcctacctgcagctcagcagcctgaca
265   ------------------------------------------------------
      tattgtcgactgtgtaggaggttgtgtcggatggacgtcgagtcgtcggactgt

      I  T  A  D  T  S  S  N  T  A  Y  L  Q  L  S  S  L  T
                                                FR3
```

FIG. 12A

```
    tctgaggacactgccgtctatttctgtgctagagagggatattatggtaactac
319 ------------------------------------------------------
    agactcctgtgacggcagataaagacacgatctctccctataataccattgatg

    S  E  D  T  A  V  Y  F  C  A  R][E  G  Y  Y  G  N  Y
                                              CDR3

    ggggtctatgctatggactactggggtcaaggaacctcagtcaccgtctcctca
373 ------------------------------------------------------
    ccccagatacgatacctgatgaccccagttccttggagtcagtggcagaggagt

    G  V  Y  A  M  D  Y][W  G  Q  C  T  S  V  T  V  S  S]

    gccaaaacgacacccccatctgtctatccactggcccgggatcc
427 --------------------------------------------
    cggttttgctgtgggggtagacagataggtgaccgggccctagg

    S  S]
```

FIG. 12B

```
               FR1                      CDR1          FR2           CDR2
                  1         2              3             4          5
        12345678901234567890123 45678901234 567890123456789 0123456
         *                       *********               *  ***
21.6    DIQMTQSPSSLSASLGGKVTITC KTSQDINKYMA WYQHKPGKRPRLLIH YTSALQP

REI     DIQMTQSPSSLSASVGDRVTITC QASQDIIKYLN WYQQTPGKAPKLLIY EASNLQA

La      DIQMTQSPSSLSASVGDRVTITC KTSQDINKYMA WYQQTPGKAPRLLIH YTSALQP

Lb      ----------------------- ----------- ----------R---- -------


                    FR3                          CDR3      FR4
           6         7         8         9         10
        78901234567890123456789012345678 901234567 8901234567
               *      *                   *******
21.6    GIPSRFSGSGSGRDYSFNISNLEPEDIATYYC LQYDNL-WT FGGGTKLEIK

REI     GVPSRFSGSGSGTDYTFTISSLQPEDIATYYC QQYQSLPYT FGQGTKLQIT

La      GIPSRFSGSGSGRDYTFTISSLQPEDIATYYC LQYDNL-WT FGQGTKVEIK

Lb      -I----------R------------------- --------- ------VE-K
```

FIG. 13

```
                      FR1                       CDR1        FR2              CDR2
                1            2             3               4             5              6
      123456789012345678901234567890 12345 67890123456789 012A3456789012345
                               ***** **  *                   ****
21.6  EVQLQQSGAELVKPGASVKLSCTASGFNIK DTYIH CVKQRPEQGLEWIG RIDPANGYTKYDPKFQG
2*CL  QVQLVQSGAEVKKPGASVKVSCKASGYTFT SYAMH WVRQAPGQRLEWMG WINAGNGNTKYSQKFQG
Ha    QVQLVQSGAEVKKPGASVKVSCKASGFNIK DTYIH WVRQAPGQRLEWMB RIDPANGYTKYDPKFQG
Hb    --------------------------FNIK ----- --------G----- -----------------
Hc    --------------------------FNIK ----- -------------- -----------------

                        FR3                    CDR3         FR4
       7            8            9            10                11
      678901234567890 12ABC345678901234 567890ABCDEF12 34567890123
          *                         *
21.6  KATITADTSSNTAYLQLSSLTSEDTAVYFCAR EGYYGNYGVYAMDY WGQGTSVTVSS
2*CL  RVTITRDTSASTAYMELSSLRSEDTAVYYCAR GGYYGSGS----NY WGQGTLVTVSS
Ha    RVTITADTSASTAYMELSSLRSEDTAVYYCAR EGYYGNYGVYAMDY WGQGTLVTVSS
Hb    -----A-------------------------- -------------- -----------
Hc    -----A-------------------------- ---F---------- -----------
```

FIG. 14

```
    HindIII KOZAK SEQUENCE
     aagcttgccgccaccatgagaccgtctattcagttcctggggctcttgttgttc
  1  ------------------------------------------------------
     ttcgaacggcggtggtactctggcagataagtcaaggaccccgagaacaacaag

                     [M  R  P  S  I  Q  F  L  G  L  L  L  F
                                                 LEADER

     tggcttcatggtgctcagtgtgacatccagatgacacagtctccatcctcactg
 55  ------------------------------------------------------
     accgaagtaccacgagtcacactgtaggtctactgtgtcagaggtaggagtgac

     W  L  H  G  A  Q  C][D  I  Q  M  T  Q  S  P  S  S  L
                                                       FR1

     tctgcatctGTAggaGATAGAgtcaccatcacttgcaagacaagccaagacatt
109  ------------------------------------------------------
     agacgtagaCATcctCTATCTcagtggtagtgaacgttctgttcggttctgtaa

     S  A  S  V  G  D  R  V  T  I  T  C][K  T  S  Q  D  I
                                                    CDR1

     aacaagtatatggcttggtaccaaCAGACAcctggaaaaGCTcctaggctgctc
163  ------------------------------------------------------
     ttgttcatataccgaaccatggttGTCTGTggaccttttCGAggatccgacgag

     N  K  Y  M  A][W  Y  Q  Q  T  P  G  K  A  P  R  L  L
                                   FR2

     atacattacacatctgcattacagccaggcatcccatcaaggttcagtggaagt
217  ------------------------------------------------------
     tatgtaatgtgtagacgtaatgtcggtccgtagggtagttccaagtcaccttca

     I  H][Y  T  S  A  L  Q  P][G  I  P  S  R  F  S  G  S
                 CDR2

     gggtctgggagagattatACTttcACCatcagcAGCctgCAGcctgaagatatt
271  ------------------------------------------------------
     cccagaccctctctaataTGAaagTGGtagtcgTCGgacGTCggacttctataa

     G  S  F  R  D  Y  T  F  T  I  S  S  L  Q  P  E  D  I
                    FR3
```

FIG. 15A

```
    gcaacttattattgtctacagtatgataatctgtggacgttcggtCAAggcacc
325 ------------------------------------------------------
    cgttgaataataacagatgtcatactattagacacctgcaagccaGTTccgtgg

    A  T  Y  Y  C][L  Q  Y  D  N  L  W  T][F  G  Q  G  T
                                CDR3                  FR4

        SPLICE DONOR SITE BamHI
    aagGTGgaaatcaaacgtgagtggatcc
379 ----------------------------
    ttcCACctttagtttgcactcacctagg

    K  V  E  I  K]
```

FIG. 15B

```
  HindIII KOZAK SEQUENCE
  AAGCTTGCCGCCACCATGGACTGGACCTGGCGCGTGTTTTGCCTGCTCGCCGTG
1 ------------------------------------------------------
  TTCGAACGGCGGTGGTACCTGACCTGGACCGCGCACAAAACGGACGAGCGGCAC

  [M D W T W R V F C L L A V
                         LEADER

   GCTCCTGGGGCCCACAGCCAGGTGCAACTAGTGCAGTCCGGCGCCGAAGTGAAG
55 ------------------------------------------------------
   CGAGGACCCCGGGTGTCGGTCCACGTTGATCACGTCAGGCCGCGGCTTCACTTC

   A P G A H S][Q V Q L V Q S G A E V K

    AAACCCGGTGCTTCCGTGAAAGTCAGCTGTAAAGCTAGCGGTttcaacattaaa
109 ------------------------------------------------------
    TTTGGGCCACGAAGGCACTTTCAGTCGACATTTCGATCGCCAaagttgtaattt

    K P G A S V K V S C K A S G F N I K][
        FR1

    gacacctatatacacTGGGTTAGACAGGCCCCtGGCCAAaGGCTgGAGTGGATg
163 ------------------------------------------------------
    ctgtggatatatgtgACCCAATCTGTCCGGgGaCCGGTTtCCGAcCTCACCTAc

    D T Y I H][W V R Q A P G Q R L E W M
     CDR1                 FR2
```

FIG. 16A

```
    GGaaggattgatcctgcgaatggttatactaaatatgacccgaagttccagggc
217 ------------------------------------------------------
    CCttcctaactaggacgcttaccaatatgatttatactgggcttcaaggtcccg

    G][R  I  D  P  A  N  G  Y  T  K  Y  D  P  K  F  Q  G][
                                 CDR2

    cgggtcACCatcACCgcaGACACCTCTgccagcACCGCCTACATGGAACTGTCC
271 ------------------------------------------------------
    gcccagTGGtagTGGcgtCTGTGGAGAcggtcgTGGCGGATGTACCTTGACAGG

    R  V  T  I  T  A  D  T  S  A  S  T  A  Y  M  E  L  S
                                                      FR3

    AGCCTGCGCTCCGAGGACACTGCAGTCTACTACTGCGCCagagagggatattat
325 ------------------------------------------------------
    TCGGACGCGAGGCTCCTGTGACGTCAGATGATGACGCGGtctctccctataata

    S  L  R  S  E  D  T  A  V  Y  Y  C  A  R][E  G  Y  Y

    ggtaactacggggtctatgctatgGACTAcTGGGGtCAaGGaACCCTTGTCACC
379 ------------------------------------------------------
    ccattgatgccccagatacgatacCTGATgACCCCaGTtCCtTGGGAACAGTGG

    G  N  Y  G  V  Y  A  M  D  Y][W  G  Q  G  T  L  V  T
       CDR3                                         FR4

    SPLICE DONOR SITE BamHI
    GTCtccTCAGGTGAGTGGATCC
433 ----------------------
    CAGaggAGTCCACTCACCTAGG

    V  S  S]
```

FIG. 16B

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 109 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein

N - Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Asp Ile Ser Asn
Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gly Ser Pro Lys Leu Leu
Ile Tyr Tyr Ala Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser
Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu
Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro
Pro Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys - C

FIG. 17A

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 114 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein

```
N - Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
    Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ser Leu Val Xaa
    Xaa Ser Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys
    Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Glu Ser Gly Val
    Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
    Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
    Tyr Asn Ser Leu Pro Glu Trp Thr Phe Gly Gln Gly Thr Lys Val Glu
    Ile Lys - C
```

FIG. 17B

```
(i)  SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 125 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein

N - Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
    Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr
    Tyr Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
    Gly Arg Ile Asp Pro Ala Asn Gly Asn Thr Lys Tyr Asp Pro Lys Phe
    Gln Gly Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr
    Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
    Ala Arg Gly Tyr Tyr Tyr Tyr Asp Ser Xaa Val Gly Tyr Tyr Ala Met
    Asp Tyr Trp Gly Gln Gly Thr Xaa Val Thr Val Ser Ser - C
```

FIG. 18A

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

```
N - Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
    Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
    Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
    Gly Trp Ile Asn Pro Tyr Gly Asn Gly Asp Thr Asn Tyr Ala Gln Lys
    Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Ser Thr Ala
    Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr
    Cys Ala Arg Ala Pro Gly Tyr Gly Ser Gly Gly Gly Cys Tyr Arg Gly Asp
    Tyr Xaa Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser - C
```

FIG. 18B